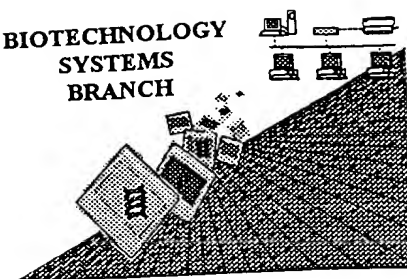


F. Hamud

## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/167,705  
Art Unit / Team No. : 1646  
Date Processed by STIC: 8/31/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/167,205

TN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- \_\_\_ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- \_\_\_ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- \_\_\_ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.
- \_\_\_ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- \_\_\_ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- \_\_\_ Variable Length

Sequence(s) \_\_\_ contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- \_\_\_ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- \_\_\_ Skipped Sequences (OLD RULES)

Sequence(s) \_\_\_ missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xI) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- \_\_\_ Skipped Sequences (NEW RULES)

Sequence(s) \_\_\_ missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- \_\_\_ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- \_\_\_ Use of <213>Organism (NEW RULES)

Sequence(s) \_\_\_ are missing this mandatory field or its response.
- \_\_\_ Use of <220>Feature (NEW RULES)

Sequence(s) \_\_\_ are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- \_\_\_ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

F. Hamid

1646

AGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/167,705

DATE: 09/02/1999  
TIME: 13:12:04

Input Set: I167705.RAW

This Raw Listing contains the General Information Section and up to first 5 pages. <sup>Denotation</sup> <sup>Corrected Diskette</sup> <sup>Comply</sup> <sup>Needed</sup>

1 <110> APPLICANT: Schmidt, Ann Marie  
2 Stern, David  
3 <120> TITLE OF INVENTION: EXTRACELLULAR NOVEL RAGE BINDING PROTEIN (EN-RAGE) AND  
4 USES THEREOF  
5 <130> FILE REFERENCE: 0575-55873  
6 <140> CURRENT APPLICATION NUMBER: US/09/167,705  
7 <141> CURRENT FILING DATE: 1998-10-06  
8 <160> NUMBER OF SEQ ID NOS: 6  
9 <170> SOFTWARE: PatentIn Ver. 2.0  
10 <210> SEQ ID NO 1  
11 <211> LENGTH: 395  
12 <212> TYPE: DNA  
13 <213> ORGANISM: SEQ1  
14 <400> SEQUENCE: 1  
15 atgactaagc tggaggacca cctggaggga atcatcaaca tcttcacca gtactccgtt 60  
16 cgggtggggc atttcgacac cctcaacaag cgtgagctga agcagctgat cacaaaggga 120  
17 acttcccaaa accctccaga acaccaaaga ccaacctacc attgacaaaa tattccaaga 180  
18 cctggatgcc gataaagacg gagccgtcag ctttgaggaa ttcgtagtcc tgggtgtccag 240  
19 ggtgctgaaa acagcccaca tagatatcca caaagagtag gtttccagca atgttcccaa 300  
20 gaagacttac ctttctcttc cctgaggctg ctccccgagg gagagagaat tataaacgta 360  
21 ctttggcaaa ttcttagcaa aaaaaaaaaa aaaaa 395  
22 <210> SEQ ID NO 2  
23 <211> LENGTH: 50  
24 <212> TYPE: PRT  
25 <213> ORGANISM: SEQ2  
26 <400> SEQUENCE: 2  
27 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Gly His Gln  
28 1 5 10 15  
29 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Tyr Glu Leu  
30 20 25 30  
31 Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Xaa Lys  
32 35 40 45  
33 Asp Gln  
34 50  
35 <210> SEQ ID NO 3  
36 <211> LENGTH: 90  
37 <212> TYPE: PRT  
38 <213> ORGANISM: SEQ3  
39 <400> SEQUENCE: 3  
40 Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln  
41 1 5 10 15  
42 Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu  
43 20 25 30  
44 Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys

? The only valid responses, per sequence  
Rules, are: Artificial Sequence, Unknown, or  
Scientific name (Genus/Species)  
see circled portion of item 12 on Error summary sheet  
see item 10 on Error summary sheet

1646

GE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/167,705

DATE: 09/02/1999  
TIME: 13:12:04

Input Set: I167705.RAW

```

45          35          40          45
46    Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
47          50          55          60
48    Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
49          65          70          75          80
50    Leu Lys Thr Ala His Ile Asp Ile His Lys
51          85          90
52    <210> SEQ ID NO 4
53    <211> LENGTH: 90
54    <212> TYPE: PRT
55    <213> ORGANISM: SEQ4
56    <400> SEQUENCE: 4
57    Thr Lys Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln
58          1          5          10          15
59    Tyr Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu
60          20          25          30
61    Lys Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys
62          35          40          45
63    Asp Gln Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys
64          50          55          60
65    Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
66          65          70          75          80
67    Leu Lys Thr Ala His Ile Asp Ile His Lys
68          85          90
69    <210> SEQ ID NO 5
70    <211> LENGTH: 18
71    <212> TYPE: PRT
72    <213> ORGANISM: SEQ5
73    <400> SEQUENCE: 5
74    Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val
75          1          5          10          15
76    Leu Lys
77    <210> SEQ ID NO 6
78    <211> LENGTH: 5
79    <212> TYPE: PRT
80    <213> ORGANISM: SEQ6
81    <400> SEQUENCE: 6
82    Ala Gln Asn Ile Thr
83          1          5

```

AGE: 3

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/167,705

DATE: 09/02/1999  
TIME: 13:12:04

Input Set: I167705.RAW

ne ? Error/Warning

Original Text

-----  
31 W "N" or "Xaa" used: Feature required

-----  
Lys Gln Leu Gly Thr Lys Glu Leu Pro Lys T

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821-1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821.825. Applicant's attention is directed to these regulations, published at 114-29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of marked-up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7. Other: \_\_\_\_\_

**Applicant must provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.